



Leu Lys Leu Leu Asn Ile Phe Lys Leu Pro Asp Trp Asn Phe Phe Asp
60 65 70

tgt cca aat ata aat tat gat aat att att tat tat tct tct att tta	292
Cys Pro Asn Ile Asn Tyr Asp Asn Ile Ile Tyr Tyr Ser Ser Ile Leu	
75 80 85	
aaa gat aat aat tta ata tat tat tta aaa aat aat tta aat att gaa	340
Lys Asp Asn Asn Leu Ile Tyr Tyr Leu Lys Asn Asn Leu Asn Ile Glu	
90 95 100 105	
ttt tta gat agt ata tta ata aaa aat aat tct ata gat att ata ttt	388
Phe Leu Asp Ser Ile Leu Ile Lys Asn Asn Ser Ile Asp Ile Ile Phe	
110 115 120	
gat agt atg tct att tta cat act aca caa tat ttt tta aaa aaa tth	436
Asp Ser Met Ser Ile Leu His Thr Thr Gln Tyr Phe Leu Lys Lys Xaa	
125 130 135	
gga ata att ttt tta cct tta ttt gat att ata ttt aaa tat cct tta	484
Gly Ile Ile Phe Leu Pro Leu Phe Asp Ile Ile Phe Lys Tyr Pro Leu	
140 145 150	
tta ata aaa aaa tat tta ggt act att att tct tat aaa gat aat ttt	532
Leu Ile Lys Lys Tyr Leu Gly Thr Ile Ile Ser Tyr Lys Asp Asn Phe	
155 160 165	
ttt gct aat att aat tca ata ata ttt agt gaa gga tct ttt tgt tat	580
Phe Ala Asn Ile Asn Ser Ile Ile Phe Ser Glu Gly Ser Phe Cys Tyr	
170 175 180 185	
ata cct aaa tat gta aag tgt aat ttt aat tta tca aca tat ttt aaa	628
Ile Pro Lys Tyr Val Lys Cys Asn Phe Asn Leu Ser Thr Tyr Phe Lys	
190 195 200	
act aat tct tct gat ttt gca caa ttt gaa cgt act tta ata ata gtt	676
Thr Asn Ser Ser Asp Phe Ala Gln Phe Glu Arg Thr Leu Ile Ile Val	
205 210 215	
ggt aaa tat tct tat gta tca tat tta gaa gga tgt aca gct tca tta	724
Gly Lys Tyr Ser Tyr Val Ser Tyr Leu Glu Gly Cys Thr Ala Ser Leu	
220 225 230	
tat aaa gaa tca caa tta cat gta gct ata gta gaa ata ata gta aaa	772
Tyr Lys Glu Ser Gln Leu His Val Ala Ile Val Glu Ile Ile Val Lys	
235 240 245	
gat tat ggt tat ata aaa tat tat aca tta caa aat tgg tat aga gga	820
Asp Tyr Gly Tyr Ile Lys Tyr Tyr Thr Leu Gln Asn Trp Tyr Arg Gly	
250 255 260 265	
gat tat tta ggt aat ggt ggt tta tat aat ttt aca act aaa cgt ggt	868
Asp Tyr Leu Gly Asn Gly Gly Leu Tyr Asn Phe Thr Thr Lys Arg Gly	
270 275 280	
ata tgt tta aat tat tca aaa tta gat tgg ata caa gtt gaa gta ggt	916
Ile Cys Leu Asn Tyr Ser Lys Leu Asp Trp Ile Gln Val Glu Val Gly	
285 290 295	

tcg att ata aca tgg aaa tac cct tct act att tta aaa ggt aaa ttt	964
Ser Ile Ile Thr Trp Lys Tyr Pro Ser Thr Ile Leu Lys Gly Lys Phe	
300 305 310	
tct att agt aat ttt tat tca ata tct ttt ata tca aat atg caa ata	1012
Ser Ile Ser Asn Phe Tyr Ser Ile Ser Phe Ile Ser Asn Met Gln Ile	
315 320 325	
gct gat act ggt agt aaa atg tat cat ata gga tct tat act aaa agt	1060
Ala Asp Thr Gly Ser Lys Met Tyr His Ile Gly Ser Tyr Thr Lys Ser	
330 335 340 345	
tat ata att tct aaa agt ata tct tta aat aac tca tta aat ata ttt	1108
Tyr Ile Ile Ser Lys Ser Ile Ser Leu Asn Asn Ser Leu Asn Ile Phe	
350 355 360	
aga ggt tta gta tat att aaa cct ttt tca tat aaa tct tat aat tat	1156
Arg Gly Leu Val Tyr Ile Lys Pro Phe Ser Tyr Lys Ser Tyr Asn Tyr	
365 370 375	
act gaa tgt agt tct tta ata ttt ggt aat aat tct tta aca gta act	1204
Thr Glu Cys Ser Ser Leu Ile Phe Gly Asn Asn Ser Leu Thr Val Thr	
380 385 390	
att cct tat ata aaa aat tat aat aat act agt tat gta aaa caa gaa	1252
Ile Pro Tyr Ile Lys Asn Tyr Asn Asn Thr Ser Tyr Val Lys Gln Glu	
395 400 405	
gct ttt gtt tct aaa att gaa ath ata tat tta ttt tta tta atg caa	1300
Ala Phe Val Ser Lys Ile Glu Ile Ile Tyr Leu Phe Leu Leu Met Gln	
410 415 420 425	
cgt ggt tta agt att tca gag tct att tca tta tta att ata ggt ttt	1348
Arg Gly Leu Ser Ile Ser Glu Ser Ile Ser Leu Leu Ile Ile Gly Phe	
430 435 440	
tgt tct gat att tat aat aaa tta ccg ttt gaa ttt aat tta gag ata	1396
Cys Ser Asp Ile Tyr Asn Lys Leu Pro Phe Glu Phe Asn Leu Glu Ile	
445 450 455	
cct ata tta ttt tca tta aaa att aaa gat ata ttt aat taattaaat	1444
Pro Ile Leu Phe Ser Leu Lys Ile Lys Asp Ile Phe Asn	
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<211> 1443

<212> DNA

<213> Synechocystis PCC6803

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<221> CDS

<222> (1)..(1443)

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ggc	ttt	gtc	acc	aac	att	gaa	gcg	gat	gct	atc	ccc	cgt	ggg	ctg	agt	96
Gly	Phe	Val	Thr	Asn	Ile	Glu	Ala	Asp	Ala	Ile	Pro	Arg	Gly	Leu	Ser	
			20					25					30			
gaa	gac	gtg	gtg	cga	ctc	att	tct	gct	aag	aaa	aat	gaa	ccc	gaa	ttc	144
Glu	Asp	Val	Val	Arg	Leu	Ile	Ser	Ala	Lys	Lys	Asn	Glu	Pro	Glu	Phe	
		35					40					45				
atg	ttg	gat	ttt	cgc	ctc	cgg	gcc	tac	cgg	cat	tgg	ctg	acc	atg	gcg	192
Met	Leu	Asp	Phe	Arg	Leu	Arg	Ala	Tyr	Arg	His	Trp	Leu	Thr	Met	Ala	
	50					55				60						
gaa	ccc	act	tgg	ccg	gcg	gtg	cat	tat	ccc	ccc	att	gat	tac	caa	gat	240
Glu	Pro	Thr	Trp	Pro	Ala	Val	His	Tyr	Pro	Pro	Ile	Asp	Tyr	Gln	Asp	
65					70				75					80		
att	att	tac	tac	tcc	gcc	cct	aag	caa	agt	aag	aaa	aaa	cta	gaa	agc	288
Ile	Ile	Tyr	Tyr	Ser	Ala	Pro	Lys	Gln	Ser	Lys	Lys	Lys	Leu	Glu	Ser	
				85				90					95			
tta	gat	gaa	gtg	gac	cca	gct	ttg	ttg	gaa	acc	ttt	gaa	aaa	tta	ggg	336
Leu	Asp	Glu	Val	Asp	Pro	Ala	Leu	Leu	Glu	Thr	Phe	Glu	Lys	Leu	Gly	
			100					105					110			
att	ccc	cta	tcg	gag	caa	aaa	cgt	tta	agt	aat	gtg	gcg	gta	gat	gcc	384
Ile	Pro	Leu	Ser	Glu	Gln	Lys	Arg	Leu	Ser	Asn	Val	Ala	Val	Asp	Ala	
		115					120					125				
att	ttt	gac	agt	gtt	tcc	att	ggc	aca	act	ttt	aag	gaa	aag	cta	gcg	432
Ile	Phe	Asp	Ser	Val	Ser	Ile	Gly	Thr	Thr	Phe	Lys	Glu	Lys	Leu	Ala	
	130					135					140					
gaa	gac	ggg	gta	att	ttc	tgt	tct	att	tct	gaa	gca	ttg	cag	gaa	cat	480
Glu	Asp	Gly	Val	Ile	Phe	Cys	Ser	Ile	Ser	Glu	Ala	Leu	Gln	Glu	His	
145					150				155					160		
ccc	gac	ctg	gtg	caa	aaa	tat	ttg	ggc	agt	gtg	gtg	ccc	acc	gcc	gac	528
Pro	Asp	Leu	Val	Gln	Lys	Tyr	Leu	Gly	Ser	Val	Val	Pro	Thr	Ala	Asp	
			165					170					175			
aac	ttc	ttt	gcc	gcc	tta	aac	tct	gct	gta	ttt	agt	gac	ggg	tcc	ttt	576
Asn	Phe	Phe	Ala	Ala	Leu	Asn	Ser	Ala	Val	Phe	Ser	Asp	Gly	Ser	Phe	
			180					185					190			
gtt	ttt	att	ccc	aaa	ggg	gtg	aag	tgt	ccc	atg	gaa	ttg	tcc	acc	tat	624
Val	Phe	Ile	Pro	Lys	Gly	Val	Lys	Cys	Pro	Met	Glu	Leu	Ser	Thr	Tyr	
		195					200					205				
ttc	cgc	att	aat	aat	ggg	gat	acg	ggg	cag	ttt	gag	cgg	aca	tta	att	672
Phe	Arg	Ile	Asn	Asn	Gly	Asp	Thr	Gly	Gln	Phe	Glu	Arg	Thr	Leu	Ile	
	210					215					220					
att	gcc	gaa	gaa	ggg	gct	tcc	gtt	agc	tat	ttg	gaa	ggg	tgt	act	gcg	720
Ile	Ala	Glu	Glu	Gly	Ala	Ser	Val	Ser	Tyr	Leu	Glu	Gly	Cys	Thr	Ala	

225	230	235	240	
ccc atg tat gac acc aat caa ctt cat gcg gcg gtg gtg gaa ttg gta				768
Pro Met Tyr Asp Thr Asn Gln Leu His Ala Ala Val Val Glu Leu Val				
	245	250	255	
gct cta gat aat gct gac att aaa tat tcc acc gta caa aac tgg tac				816
Ala Leu Asp Asn Ala Asp Ile Lys Tyr Ser Thr Val Gln Asn Trp Tyr				
	260	265	270	
gct ggg gac gaa aat ggc aag ggc gga att tac aac ttt gtg act aaa				864
Ala Gly Asp Glu Asn Gly Lys Gly Gly Ile Tyr Asn Phe Val Thr Lys				
	275	280	285	
cgg ggt cta tgt aaa gga gtt aat tcc aaa att tcc tgg acc caa gta				912
Arg Gly Leu Cys Lys Gly Val Asn Ser Lys Ile Ser Trp Thr Gln Val				
	290	295	300	
gaa acc ggt tcc gcc att acc tgg aaa tac ccc agt tgt gtg cta gtt				960
Glu Thr Gly Ser Ala Ile Thr Trp Lys Tyr Pro Ser Cys Val Leu Val				
	305	310	315	320
ggg gat aat tcc gtc ggg gaa ttc tac tct att gct tta act aac aac				1008
Gly Asp Asn Ser Val Gly Glu Phe Tyr Ser Ile Ala Leu Thr Asn Asn				
	325	330	335	
aaa cag caa gct gat acg gga act aaa atg att cac atc ggt aaa aat				1056
Lys Gln Gln Ala Asp Thr Gly Thr Lys Met Ile His Ile Gly Lys Asn				
	340	345	350	
acc cgt agt atc att att tcc aaa ggc att tcc gct ggt aat tcc gcc				1104
Thr Arg Ser Ile Ile Ile Ser Lys Gly Ile Ser Ala Gly Asn Ser Ala				
	355	360	365	
aac agt tac cgg ggt ttg gtg aaa atg gga cct aaa gcc cag ggc gct				1152
Asn Ser Tyr Arg Gly Leu Val Lys Met Gly Pro Lys Ala Gln Gly Ala				
	370	375	380	
cgc aat tat tcc cag tgt gat tcc atg ctc att ggc gat cgg gca gcg				1200
Arg Asn Tyr Ser Gln Cys Asp Ser Met Leu Ile Gly Asp Arg Ala Ala				
	385	390	395	400
gct aat act ttt ccc tat att caa gtg gac aat aat acc gcc aaa gta				1248
Ala Asn Thr Phe Pro Tyr Ile Gln Val Asp Asn Asn Thr Ala Lys Val				
	405	410	415	
gaa cat gaa gct tcc act tcc aaa att ggc gag gat caa ctc ttt tac				1296
Glu His Glu Ala Ser Thr Ser Lys Ile Gly Glu Asp Gln Leu Phe Tyr				
	420	425	430	
ttt gcc caa cgg gga att tct gag gaa gat gcg gtg tcc atg cta gtc				1344
Phe Ala Gln Arg Gly Ile Ser Glu Glu Asp Ala Val Ser Met Leu Val				
	435	440	445	
agc ggt ttc tgt aag gat gtg cta aac gaa tta ccc atg gaa ttt gcg				1392
Ser Gly Phe Cys Lys Asp Val Leu Asn Glu Leu Pro Met Glu Phe Ala				
	450	455	460	

gcg	gag	gct	gat	aaa	tta	ctg	agt	ctc	aaa	cta	gaa	ggg	act	gtg	ggg	1440
Ala	Glu	Ala	Asp	Lys	Leu	Leu	Ser	Leu	Lys	Leu	Glu	Gly	Thr	Val	Gly	
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taa 1443

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 <213> Escherichia coli

<220>
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1				5				10						15		
aat	act	gaa	gca	act	gac	gat	gtc	aaa	acc	tgg	acc	ggc	ggc	ccg	ctg	96
Asn	Thr	Glu	Ala	Thr	Asp	Asp	Val	Lys	Thr	Trp	Thr	Gly	Gly	Pro	Leu	
			20					25						30		
aat	tat	aaa	gaa	gga	ttc	ttc	acc	cag	tta	gcc	acc	gat	gag	ctg	gca	144
Asn	Tyr	Lys	Glu	Gly	Phe	Phe	Thr	Gln	Leu	Ala	Thr	Asp	Glu	Leu	Ala	
		35					40					45				
aag	ggg	ata	aac	gaa	gag	gtg	gtg	cgc	gca	att	tcg	gcg	aag	cgt	aat	192
Lys	Gly	Ile	Asn	Glu	Glu	Val	Val	Arg	Ala	Ile	Ser	Ala	Lys	Arg	Asn	
	50					55					60					
gag	ccg	gag	tgg	atg	ctg	gag	ttt	cgt	cta	aac	gcc	tat	cgc	gca	tgg	240
Glu	Pro	Glu	Trp	Met	Leu	Glu	Phe	Arg	Leu	Asn	Ala	Tyr	Arg	Ala	Trp	
65					70					75					80	
ctg	gag	atg	gaa	gaa	ccg	cac	tgg	ttg	aaa	gcg	cac	tac	gac	aag	ctg	288
Leu	Glu	Met	Glu	Glu	Pro	His	Trp	Leu	Lys	Ala	His	Tyr	Asp	Lys	Leu	
				85					90					95		
aat	tat	cag	gat	tac	agc	tac	tac	tca	gca	cca	tcg	tgc	ggg	aat	tgt	336
Asn	Tyr	Gln	Asp	Tyr	Ser	Tyr	Tyr	Ser	Ala	Pro	Ser	Cys	Gly	Asn	Cys	
			100					105					110			
gac	gac	act	tgc	gcg	tct	gaa	cct	ggc	gcg	gtg	cag	caa	act	ggc	gcg	384
Asp	Asp	Thr	Cys	Ala	Ser	Glu	Pro	Gly	Ala	Val	Gln	Gln	Thr	Gly	Ala	
		115					120					125				
aac	gcc	ttt	tta	agt	aaa	gag	gtg	gag	gcg	gcg	ttt	gag	cag	ttg	ggc	432
Asn	Ala	Phe	Leu	Ser	Lys	Glu	Val	Glu	Ala	Ala	Phe	Glu	Gln	Leu	Gly	
	130					135					140					
gtt	ccc	gtg	cgg	gaa	ggc	aaa	gag	gtg	gcg	gtg	gat	gcc	att	ttc	gac	480
Val	Pro	Val	Arg	Glu	Gly	Lys	Glu	Val	Ala	Val	Asp	Ala	Ile	Phe	Asp	

145		150		155		160	
tca gtt tcg gtt gcc act act tat cgc gaa aaa ctg gcg gag cag gga	528						
Ser Val Ser Val Ala Thr Thr Tyr Arg Glu Lys Leu Ala Glu Gln Gly							
165		170		175			
att att ttc tgt tcc ttt ggt gag gcg atc cac gat cac ccg gaa ctg	576						
Ile Ile Phe Cys Ser Phe Gly Glu Ala Ile His Asp His Pro Glu Leu							
180		185		190			
gtg cgt aaa tat ctc ggc acc gtg gtg ccg ggg aat gac aac ttc ttt	624						
Val Arg Lys Tyr Leu Gly Thr Val Val Pro Gly Asn Asp Asn Phe Phe							
195		200		205			
gcc gcg ctt aat gcg gcg gta gcc tct gat ggt acg ttt att tat gtg	672						
Ala Ala Leu Asn Ala Ala Val Ala Ser Asp Gly Thr Phe Ile Tyr Val							
210		215		220			
cct aaa ggc gtg cgc tgc ccg atg gaa ctt tcc acc tat ttt cgc att	720						
Pro Lys Gly Val Arg Cys Pro Met Glu Leu Ser Thr Tyr Phe Arg Ile							
225		230		235		240	
aac gca gaa aaa acc ggg cag ttt gag gcg acc att ctg gtg gcc gac	768						
Asn Ala Glu Lys Thr Gly Gln Phe Glu Arg Thr Ile Leu Val Ala Asp							
245		250		255			
gaa gac agc tac gtc agc tac att gaa ggc tgt tcc gct ccg gtg cgt	816						
Glu Asp Ser Tyr Val Ser Tyr Ile Glu Gly Cys Ser Ala Pro Val Arg							
260		265		270			
gac agc tat cag tta cac gcg gca gtg gtg gaa gtc atc atc cat aaa	864						
Asp Ser Tyr Gln Leu His Ala Ala Val Val Glu Val Ile Ile His Lys							
275		280		285			
aac gcc gag gtg aaa tat tcc acg gta caa aac tgg ttt cct ggc gat	912						
Asn Ala Glu Val Lys Tyr Ser Thr Val Gln Asn Trp Phe Pro Gly Asp							
290		295		300			
aac aac acc ggc ggt att ctc aac ttc gtc acc aag cgt gct ttg tgc	960						
Asn Asn Thr Gly Gly Ile Leu Asn Phe Val Thr Lys Arg Ala Leu Cys							
305		310		315		320	
gaa ggc gaa aac agc aaa atg tca tgg acg caa tca gaa acc ggg tca	1008						
Glu Gly Glu Asn Ser Lys Met Ser Trp Thr Gln Ser Glu Thr Gly Ser							
325		330		335			
gcg att acg tgg aaa tat ccc agc tgc att ttg cgc ggc gat aac tcc	1056						
Ala Ile Thr Trp Lys Tyr Pro Ser Cys Ile Leu Arg Gly Asp Asn Ser							
340		345		350			
att ggt gag ttt tac tca gtg gcg ctg acc agc ggt cat cag caa gcg	1104						
Ile Gly Glu Phe Tyr Ser Val Ala Leu Thr Ser Gly His Gln Gln Ala							
355		360		365			
gat acc ggc acc aag atg atc cac atc ggt aaa aac acc aaa tcg acc	1152						
Asp Thr Gly Thr Lys Met Ile His Ile Gly Lys Asn Thr Lys Ser Thr							
370		375		380			

att atc tcg aaa ggg atc tct gcc gga cat agt cag aac agt tat cgc	1200
Ile Ile Ser Lys Gly Ile Ser Ala Gly His Ser Gln Asn Ser Tyr Arg	
385 390 395 400	
ggc tta gtg aaa atc atg ccg acg gca acc aat gcg cgc aat ttc act	1248
Gly Leu Val Lys Ile Met Pro Thr Ala Thr Asn Ala Arg Asn Phe Thr	
405 410 415	
cag tgc gac tca atg ctg att ggc gct aat tgt ggg gcg cat acc ttc	1296
Gln Cys Asp Ser Met Leu Ile Gly Ala Asn Cys Gly Ala His Thr Phe	
420 425 430	
ccg tat gtt gag tgt cgt aac aat agt gcg caa ctg gaa cac gag gca	1344
Pro Tyr Val Glu Cys Arg Asn Asn Ser Ala Gln Leu Glu His Glu Ala	
435 440 445	
acg aca tca cgt att ggt gaa gat caa ctg ttt tac tgc ctg caa cgc	1392
Thr Thr Ser Arg Ile Gly Glu Asp Gln Leu Phe Tyr Cys Leu Gln Arg	
450 455 460	
ggg atc agc gaa gaa gac gcc atc tcg atg att gtt aac ggt ttc tgc	1440
Gly Ile Ser Glu Glu Asp Ala Ile Ser Met Ile Val Asn Gly Phe Cys	
465 470 475 480	
aaa gac gtg ttc tcg gag ctg ccg ttg gaa ttt gcc gtt gaa gca caa	1488
Lys Asp Val Phe Ser Glu Leu Pro Leu Glu Phe Ala Val Glu Ala Gln	
485 490 495	
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Lys Leu Leu Ala Ile Ser Leu Glu His Ser Val Gly	
500 505	

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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<210> 5
 <211> 26
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer

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<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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